
Image source : PROCROSS

Pilot genomic evaluations of French crossbred dairy cattle

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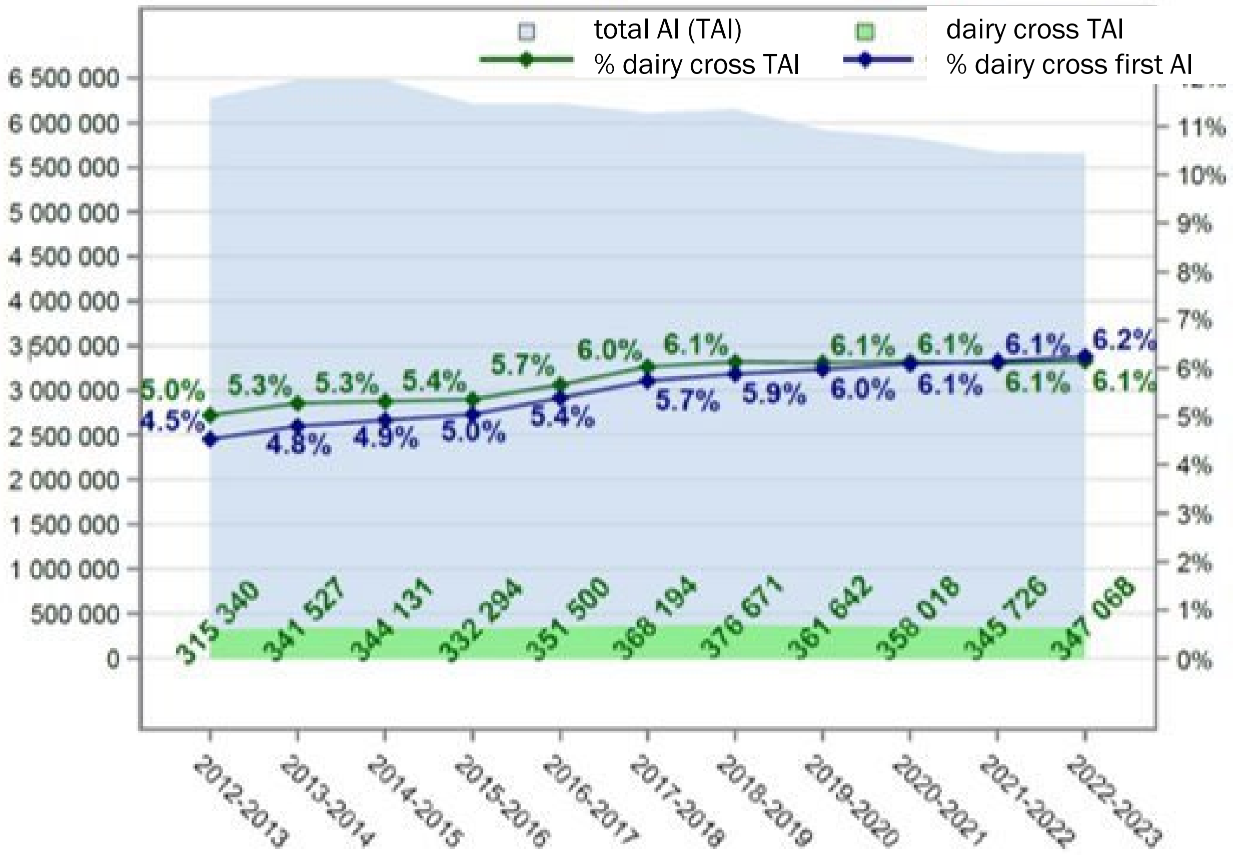
Interbull Meeting 2026

Crossbreeding in France

- **Steady increase of dairy crossbreeding artificial insemination (AI)**

- **Examples :**
  - F1 crosses from multiple breeds
  - Rotational cross : Procross (Holstein x Montbéliarde x Viking Red)
  - Kiwi crosses
  - …

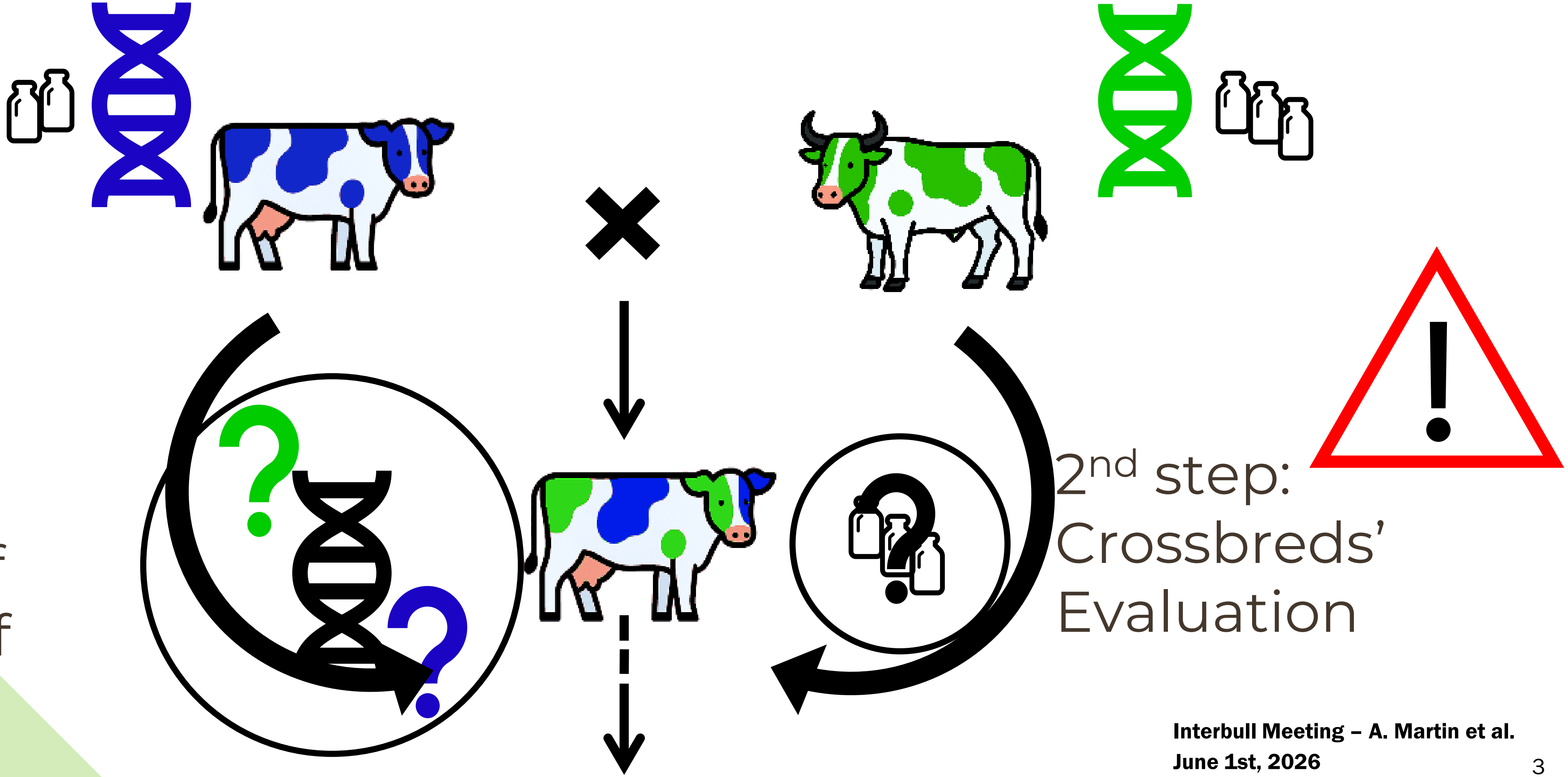
- **No genetic/genomic tools**
  → Need EBV to use for reproduction planning



Source : IDELE

→ **Transevagenoc Project**

How do we evaluate dairy crosses?



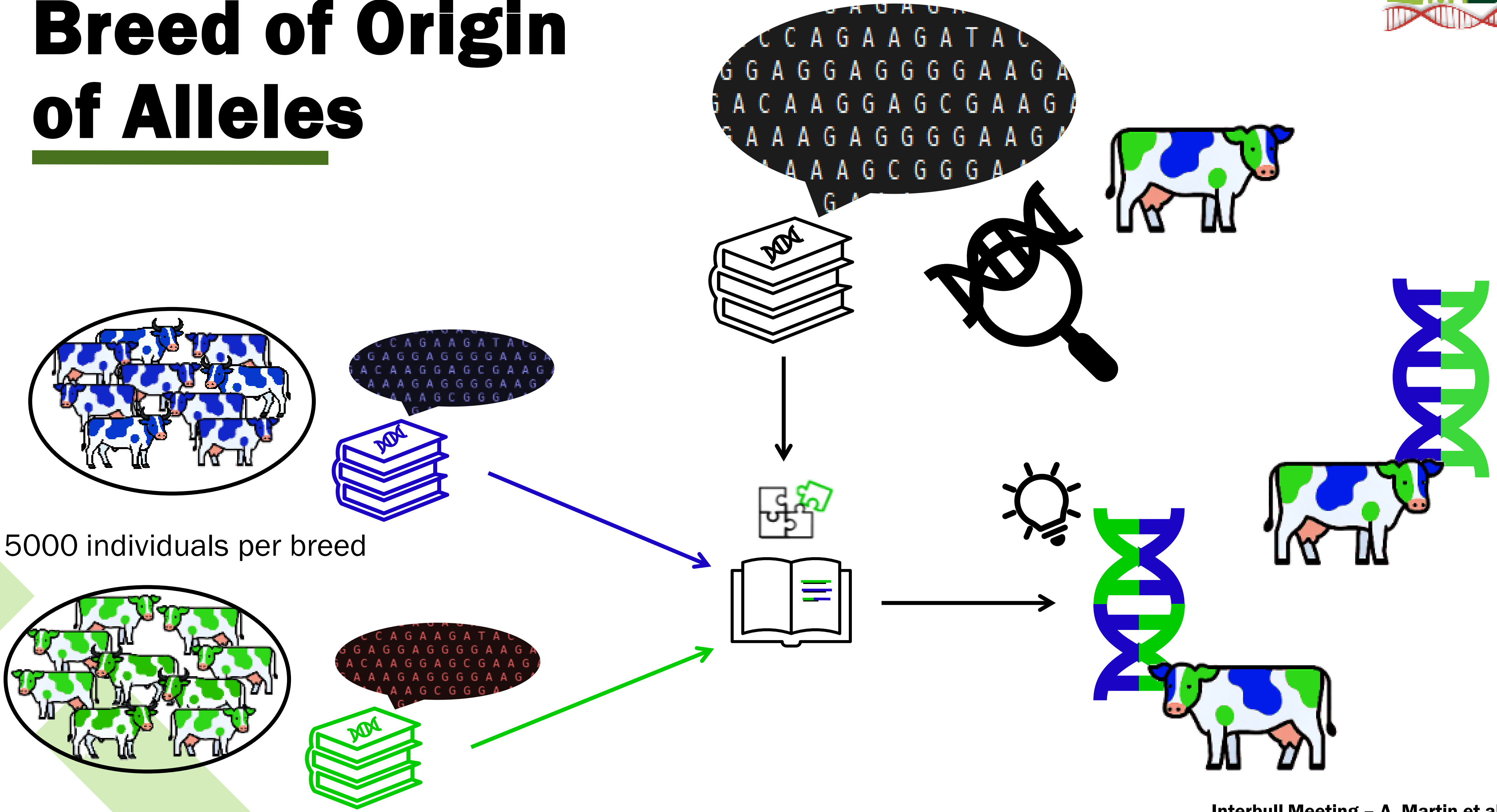
1st step:
Breed of
Origin of
Alleles

2nd step:
Crossbreds'
Evaluation

Material & Method

- **Dairy breeds : Holstein, Montbéliarde, Normande**
- **Genotypes (54K SNP) : 4,004 individuals**
- **Phenotypes : 1st lactation for**
  - Milk yield
  - Fat yield
  - Protein yield
  - Somatic Cell Score (SCS)
  - Calving To First Service (CTFS)

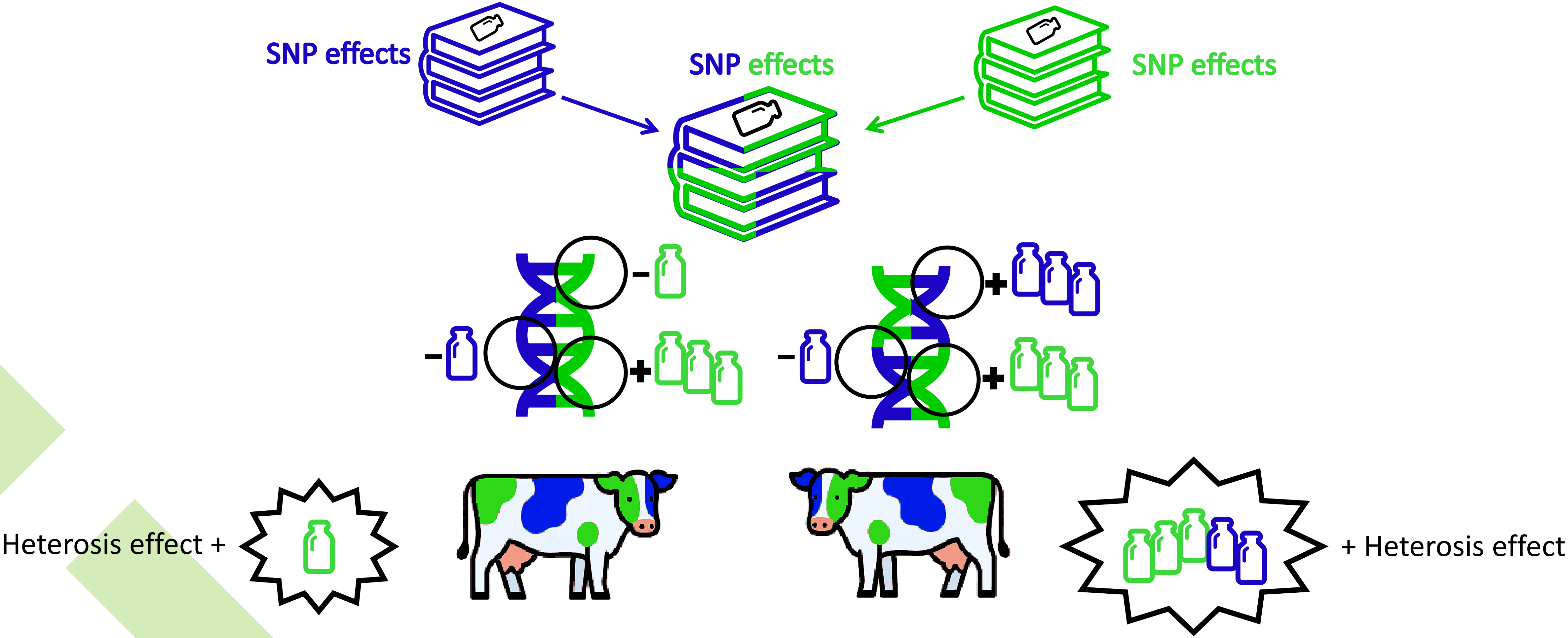
Breed of Origin of Alleles



5000 individuals per breed

Inhouse program : BreedOrigin (Didier Boichard)

IPVGeno method : Concept



SNP effects

SNP effects

SNP effects

Heterosis effect +

+ Heterosis effect

Inhouse program : CrossSG (Pascal Croiseau)

IPVGeno method : Crossbred index

$$Index_i = \sum_{b=1}^{\#\_breed}\left(\sum_{j=1}^{\#\_SNP}\left(\beta_{i,j,b} \times X_{i,j,b}\right) + p_{i,b} \times GBD_b\right) + ph_i \times H$$

$\beta_{i,j,b}$: Breed of origin of allele

$X_{i,j,b}$: Pure bred SNP effect

$p_{i,b}$: Breed composition

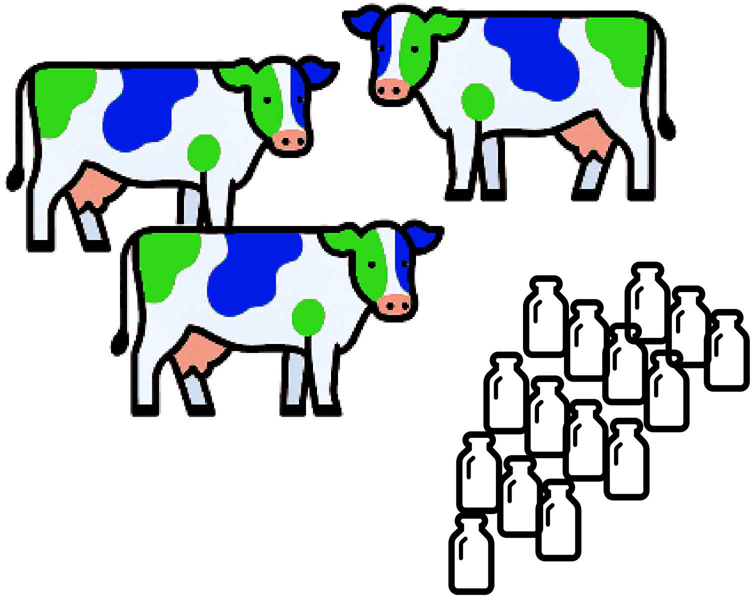
GBD_b : Genetic breed difference ← **Holstein base**

ph_i : Individual heterosis level

H : Heterosis effect

Milk yield
Raw indices

- **Correlations :**
  - (EBV, EBV+Het) = 0.99
  - (EBV, phenotypes) = 0.35
  - (EBV+Het, phenotypes) = 0.36

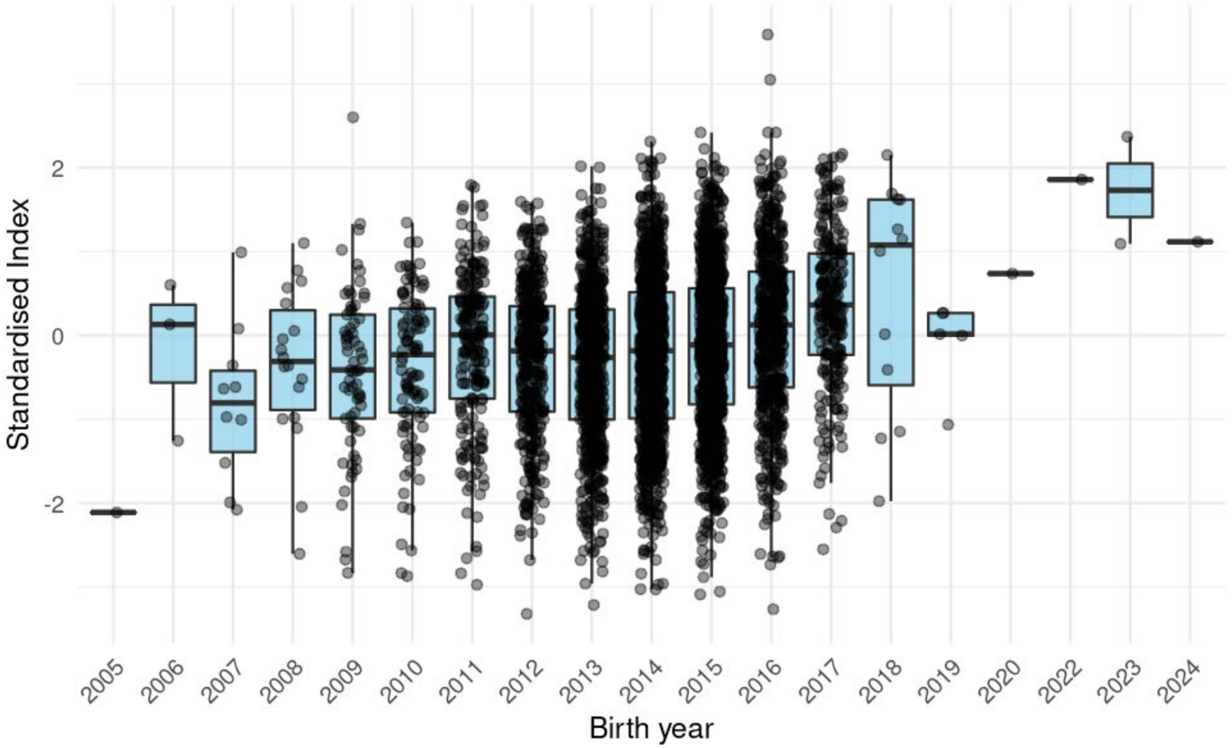


- $Corr/\sqrt{h^2}$* :
  - (EBV, phenotypes) = 0.65
  - (EBV+Het, phenotypes) = 0.66

* h^2 is the averaged heritability from the three pure breeds (= 0.30)

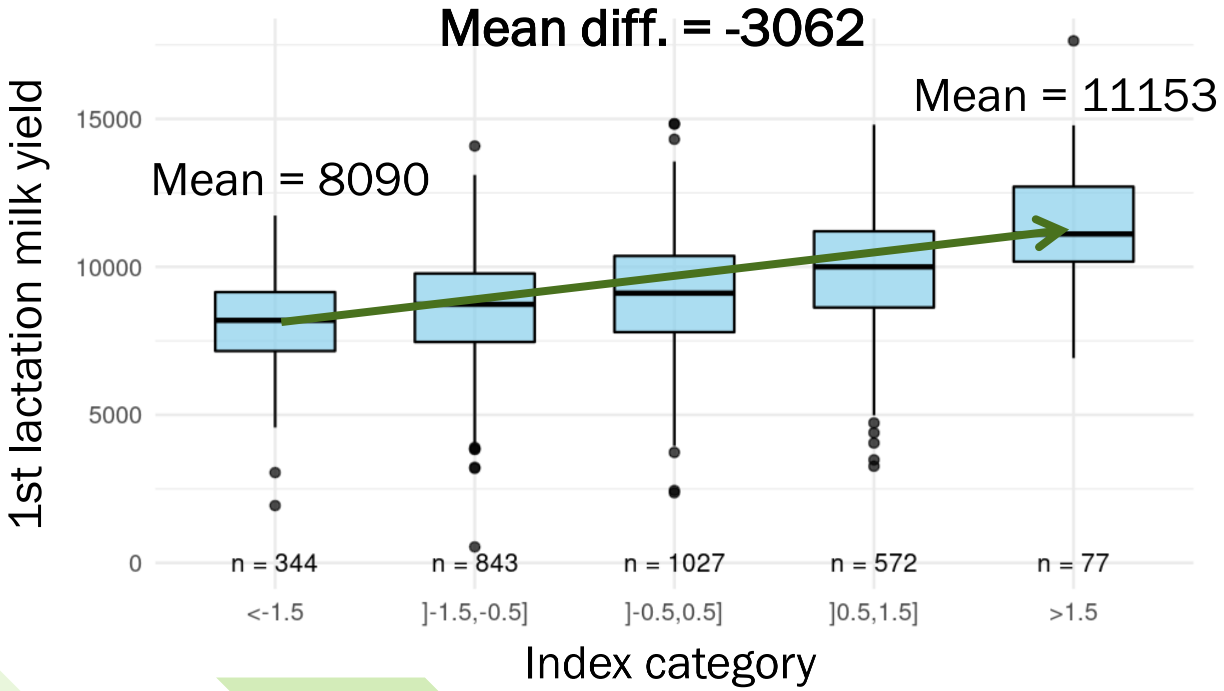
Index Standardisation

Indices are standardised on a subset of the crossbred population



Milk production

Standardised Index

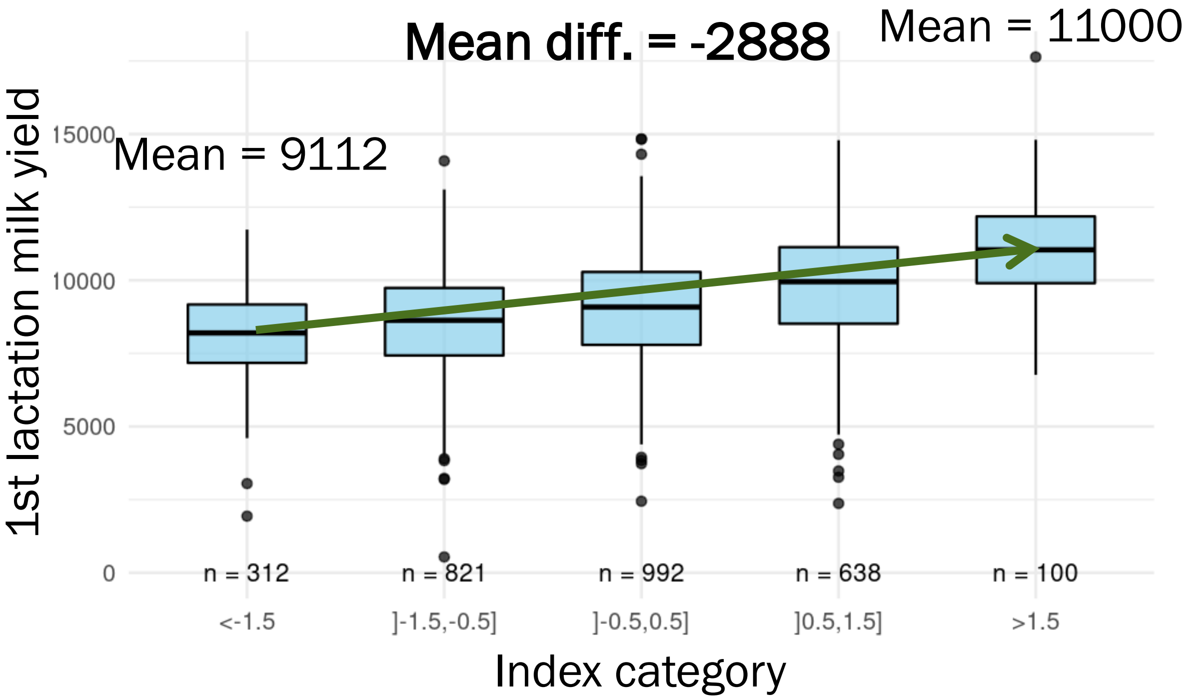


Mean diff. = -3062

Mean = 11153

Mean = 8090

Standardised Index with Heterosis



Mean diff. = -2888

Mean = 11000

Mean = 9112

Perspectives

- **Pilot evaluation to motivate the industry to collect more data**
  - IPVgeno method allowed to get useable indices

- **Evaluation of the crossbred SNP effects**
  - Simulations to estimate the necessary sample sizes for the more advanced methods → Carlos Cambraia (MSc student)

Take-home
Transevagenoc project

- **Programs were developped (BreedOrigin and CrossSG)**

- **Pilot indices for crossbred dairy cattle were made available end of 2025**
  - Routine for crossbreds from six pure breeds

- **Support the genotyping effort**
  - More data are needed !
  - Carlos Cambraia's work

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Thank you !
Any questions ?

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